

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 29, 2006, 03:02:19 ; Search time 255 Seconds  
(without alignments)  
3176.261 Million cell updates/sec

Title: US-09-824-575A-2  
Perfect score: 5981  
Sequence: 1 MSRA5VSGDLEAPATYVL.....VSQEVIRAYDTTKKSRKK 1148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

UniProt 05.80.\*

1: uniprot\_trembl.\*

2: uniprot\_trembl.\*

\*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5954	99.5	1148	1 AT9A2 HUMAN	Q9nt12 homo sapien
2	5951	99.5	1188	2 Q6ZSP3 HUMAN	Q6zsp3 homo sapien
3	5661	94.6	1148	1 AT9A2 MOUSE	P98200 mus musculus
4	4923.5	82.3	968	2 Q6ZU25 HUMAN	Q6zu25 homo sapien
5	4166.5	69.7	1164	2 Q8BR88 MOUSE	Q8br88 mus musculus
6	4166.5	69.7	1195	2 Q5DTG0 MOUSE	Q5dtg0 mus musculus
7	4157.5	69.5	1164	1 AT9A1 HUMAN	P70704 mus musculus
8	4133	69.1	1149	1 AT9A1 MOUSE	Q59ex4 homo sapien
9	4113	68.8	1177	2 Q59EX4 HUMAN	Q59ex4 homo sapien
10	4107	68.7	1149	1 AT9A1 BOVIN	Q29449 bos taurus
11	4003	66.9	1247	2 Q4RTG6 TETNG	Q4rtg6 tetraodon n
12	3372	56.4	947	2 Q4SS57 TETNG	Q4ss57 tetraodon n
13	3265	54.6	1150	2 Q87014 DROME	Q8t014 drosophila
14	3249.5	54.3	1235	2 Q9V6P5 DROME	Q9v6p5 drosophila
15	3249.5	54.3	1360	2 Q8ML69 DROME	Q8ml69 drosophila
16	3212	53.7	1076	2 Q7PMY3 ANOGA	Q7pmv3 anopheles g
17	3187.5	53.3	1216	2 Q6AWM7 DROME	Q6awm7 drosophila
18	2928.5	49.0	806	2 Q52KQ7 MOUSE	Q52kq7 mus musculus
19	2711.5	45.3	1357	2 Q4X1T4 ASPFU	Q4x1t4 aspergillus
20	2695	45.1	1348	2 Q5B018 EMENI	Q5b018 aspergillus
21	2655	44.4	1333	2 Q6C314 YARLI	Q6c314 yarrowia li
22	2642	44.2	1384	2 Q4P669 USUMA	Q4p669 ustilago ma
23	2640	44.1	1358	2 Q94296 SCHPO	Q94296 schizosacch
24	2636	44.1	1363	2 Q417R5 GIBZE	Q417r5 gibberella
25	2633.5	44.0	1305	2 Q9P424 AJRCA	Q9p424 ajellomyces
26	2610.5	43.6	1133	2 Q61P70 CABER	Q61f70 caenorhabdi
27	2600	43.5	1360	2 Q7RZL3 NEUCR	Q7rzl3 neurospora
28	2582	43.2	1343	2 Q6CY12 KLULA	Q6cy12 kluyveromyc
29	2569.5	43.0	1139	2 Q9U280 CABEL	Q9u280 caenorhabdi
30	2549.5	42.6	1320	2 Q5ADR3 CANAL	Q5adr3 candida alb
31	2535.5	42.4	1328	2 Q6FT10 CANGA	Q6ft10 candida gla

32	2513	42.0	1355	1 ATC3 YBAST	P39524 saccharomyc
33	2506.5	41.9	1089	2 Q7JK70 CABEL	Q7jk70 caenorhabdi
34	2498	41.8	1326	2 Q5KP96 CRYNE	Q5kp96 cryptococcu
35	2487	41.6	1328	2 Q55ZY9 CRYNE	Q55zy9 cryptococcu
36	2425.5	40.6	1313	2 Q55E61 DICDI	Q55e61 dictyostelli
37	2362.5	39.5	1311	2 Q759C7 ASHGO	Q759c7 ashbya goss
38	2341.5	37.5	1209	1 AT8B2 HUMAN	P98198 homo sapien
39	2239.5	37.4	1223	2 Q72486 HUMAN	Q72486 homo sapien
40	2235.5	37.4	1201	2 Q4RTU6 TETNG	Q4rtu6 tetraodon n
41	2231.5	37.3	1250	2 Q5BL50 XENTR	Q5bl50 xenopus tro
42	2225	37.2	1192	1 AT8B4 HUMAN	Q8tbf2 homo sapien
43	2223	37.2	1251	1 AT9B1 HUMAN	Q43520 homo sapien
44	2221	37.1	1213	1 ALA3 ARATH	Q9xie6 arabidopsis
45	2209	36.9	1251	2 Q6R964 MOUSE	Q6r964 mus musculu

## ALIGNMENTS

### RESULT 1

AT9A2 HUMAN

ID AT9A2 HUMAN STANDARD; PRT; 1148 AA.

AC Q9NT12; Q9NPUG; Q9NTL2; Q9NYM3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Potential phospholipid-transporting ATPase IB (EC 3.6.3.1) (ATPase

DE class I type 8A member 2) (ML-1).

GN Name=ATP8A2; Synonyms=ATPIB;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE (ISOFORM 2).

RA Sun X.L., Milo G.B., Li D.;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed15057823; DOI=10.1038/nature02379;

RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,

RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,

RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.B.,

RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,

RA Ashwell R.I.S., Babbage A.K., Baggeley C.L., Bailey J., Bannerjee R.,

RA Barlow K.P., Bates K., Beasley H., Bird C.P., Bray-Allen S.,

RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clee C.M.,

RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,

RA Deloukas P., Dhami P., Dunham I., Dunn M., Earthrowl M.E.,

RA Ellington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,

RA Garner P., Garnett J., Gilbert J.G.R., Gilson C.J., Ghori J.,

RA Graham D.V., Gribble S.M., Griffiths C., Hall R.E., Hammond S.,

RA Harley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,

RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,

RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,

RA Mashreghi-Mohammadi M., McLaren S.J., McMurray A., Milne S.,

RA Moore M.J.P., Nickerson T., Palmer S.A., Pearce A.V., Peck A.I.,

RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Searle S.,

RA Sehra H.K., Showkeen R., Skuce C.D., Smith M., Steward C.A.,

RA Sycamore N., Tester J., Thomas D.W., Tracey A., Tromans A., Tubby B.,

RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,

RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,

RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.;

RL "The DNA sequence and analysis of human chromosome 13.";

RL Nature 428:522-528(2004).

RN [3]

RP PARTIAL NUCLEOTIDE SEQUENCE.

RX MEDLINE=20017962; PubMed=10551800;

RA Sun X.L., Li D., Fang J., Noyes I., Casto B., Theil K., Shuler C.,

RA Milo G.B.;

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OM protein - protein search, using sw model

Run on: March 29, 2006, 03:11:59 ; Search time 26 seconds  
(without alignments)  
1302.290 Million cell updates/sec

Title: US-09-824-575A-2

Perfect score: 5981

Sequence: 1 MSRAVSVDQLEAPRTYL.....VSQEVIRAYDTTKKSRKK 1148

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications\_AA\_New:\*
- 1: /SIDSS/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 2: /SIDSS/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 3: /SIDSS/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 4: /SIDSS/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 5: /SIDSS/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 6: /SIDSS/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 7: /SIDSS/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 8: /SIDSS/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2236.5	37.2	1190	7	US-11-043-889-20
2	2223	37.2	1251	7	US-11-043-889-22
3	2103	35.2	1216	7	US-11-096-568A-28970
4	2079	34.8	1218	7	US-11-096-568A-31175
5	2073	34.7	1166	7	US-11-096-568A-30808
6	2073	34.7	1174	7	US-11-096-568A-30807
7	2066.5	34.6	1167	7	US-11-096-568A-30871
8	2061.5	34.5	1181	7	US-11-096-568A-27847
9	2061.5	34.5	1189	7	US-11-096-568A-27846
10	2042.5	34.1	1169	7	US-11-096-568A-31176
11	2032.5	34.0	1184	7	US-11-096-568A-29280
12	1941	32.5	1057	7	US-11-096-568A-30809
13	1939	32.4	1108	7	US-11-096-568A-28972
14	1929.5	32.3	1072	7	US-11-096-568A-27848
15	1915	32.0	1110	7	US-11-096-568A-31177
16	1897.5	31.7	1063	7	US-11-096-568A-29281
17	1797	30.0	1134	7	US-11-043-889-34
18	1759	29.4	1508	7	US-11-043-889-47
19	1753	29.3	1187	7	US-11-043-889-46
20	1733	29.0	989	7	US-11-096-568A-29282
21	1680	28.1	1588	7	US-11-043-889-37
22	1268	21.2	1194	7	US-11-000-463-249
23	1265	21.2	1070	7	US-11-000-463-721
24	1221	20.4	877	6	US-10-821-234-960
25	1047.5	17.5	756	6	US-10-330-773-731

26	1042	17.4	736	7	US-11-072-512-3774	Sequence 3774, Ap
27	1039.5	17.2	912	6	US-10-501-035-372	Sequence 372, App
28	751.5	12.6	529	7	US-11-072-512-2137	Sequence 2137, Ap
29	739.5	12.4	501	6	US-10-537-002-61	Sequence 61, Appl
30	595.5	10.0	376	7	US-11-096-568A-7703	Sequence 7703, Ap
31	556	9.3	255	6	US-10-330-773-734	Sequence 734, App
32	552.5	9.2	340	7	US-11-096-568A-7704	Sequence 7704, Ap
33	550.5	9.2	337	7	US-11-096-568A-7705	Sequence 7705, Ap
34	389.5	6.5	890	6	US-10-510-386-26	Sequence 26, Appl
35	375.5	6.3	1015	6	US-10-957-569-51	Sequence 51, Appl
36	375.5	6.3	1015	7	US-11-097-589-50	Sequence 50, Appl
37	356.5	6.0	1220	6	US-10-501-035-260	Sequence 260, App
38	327	5.5	919	7	US-11-074-176-284	Sequence 284, App
39	315.5	5.3	892	7	US-11-082-389-396	Sequence 396, App
40	307	5.1	997	6	US-10-501-035-238	Sequence 238, App
41	296	4.9	388	7	US-11-072-512-3764	Sequence 3764, Ap
42	293.5	4.9	1023	6	US-10-821-234-1377	Sequence 1377, Ap
43	198	3.3	946	7	US-11-010-239-42	Sequence 42, Appl
44	166	2.8	775	6	US-10-467-657-4032	Sequence 4032, Ap
45	142.5	2.4	1001	6	US-10-467-962B-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1

US-11-043-889-20  
; Sequence 20, Application US/11043889  
; Publication No. US2006008819A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtis, Rory A.J.  
; APPLICANT: Gluckman, Maria Alexandra  
; APPLICANT: Meyers, Rachel E.  
; TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,  
; TITLE OF INVENTION: 57259, 67118, 67067, 62092, FHS8295SL, 57255,  
; FILE OF INVENTION: AND 57255ALT MOLECULES AND USES THEREFOR  
; FILE REFERENCE: MP102-095DV10NNIM  
; CURRENT APPLICATION NUMBER: US/11/043.889  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: US 10/154,419  
; PRIOR FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 09/858194  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 60/204211  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 09/895811  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/215376  
; PRIOR FILING DATE: 2000-06-29  
; PRIOR APPLICATION NUMBER: US 09/919781  
; PRIOR FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/221769  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/957664  
; PRIOR FILING DATE: 2001-09-19  
; PRIOR APPLICATION NUMBER: US 60/233790  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: US 09/964295  
; PRIOR FILING DATE: 2001-09-25  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: FastSeq Version 4.0  
; SEQ ID NO 20  
; LENGTH: 1190  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-043-889-20

Query Match 37.2%; Score 2226.5; DB 7; Length 1190;  
Best Local Similarity 40.9%; Pred. No. 8.3e-176;  
Matches 469; Conservative 210; Mismatches 380; Indels 89; Gaps 18;

27 KPRDNRISTAKYSVLTPFLYEQIRRAAFLLAQIPDVSPGRTYTLVPLII 86

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OM protein - protein search, using sw model

Run on: March 29, 2006, 03:10:59 ; Search time 177 Seconds  
(without alignments)  
2709.989 Million cell updates/sec

Title: US-09-824-575A-2  
Perfect score: 5981  
Sequence: 1 MSRATSVGDQLEAPARTIYL.....VSQEVIRAYDTTKKSRKK 1148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues  
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5954	99.5	1176	4	US-10-041-395-2
2	5661	94.6	1148	5	US-10-732-923-22564
3	4944	82.7	994	5	US-10-732-923-22746
4	4363	72.9	883	4	US-10-041-395-5
5	4166.5	69.7	1164	5	US-10-732-923-22563
6	4157.5	69.5	1164	5	US-10-732-923-22727
7	4153.5	69.4	1161	4	US-10-170-102-4
8	4153.5	69.4	1161	5	US-10-732-923-22728
9	4133.5	69.1	1193	4	US-10-467-685-2
10	4133	69.1	1149	5	US-10-732-923-22562
11	4119	68.9	790	5	US-10-732-923-22731
12	4107	68.7	1149	5	US-10-732-923-22750
13	3793	63.4	729	5	US-10-732-923-22733
14	3302.5	55.2	1142	5	US-10-732-923-22578
15	3265	54.6	1150	5	US-10-732-923-22717
16	3249.5	54.3	1235	5	US-10-732-923-22719
17	3249.5	54.3	1360	5	US-10-732-923-22718
18	3220.5	53.8	1297	6	US-11-097-143-25221
19	3171	53.0	613	5	US-10-732-923-22739
20	2865.5	47.9	1352	5	US-10-732-923-22570
21	2640	44.1	1104	4	US-10-369-493-32548
22	2640	44.1	1258	4	US-10-310-154-703
23	2640	44.1	1258	5	US-10-732-923-621
24	2640	44.1	1258	5	US-10-732-923-22696
25	2633.5	44.0	1305	5	US-10-732-923-22697
26	2600	43.5	1360	5	US-10-732-923-22698
27	2574.5	43.0	1299	4	US-10-369-493-3557

Sequence 22712, A  
Sequence 702, App  
Sequence 1388, Ap  
Sequence 620, App  
Sequence 22760, A  
Sequence 12862, A  
Sequence 4, Appli  
Sequence 523, App  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 20, Appli  
Sequence 22, Appli  
Sequence 1210, Ap  
Sequence 70, Appli  
Sequence 22729, A  
Sequence 5289, Ap  
Sequence 22589, A

28 2569.5 43.0 1139 5 US-10-732-923-22712  
29 2513 42.0 1355 4 US-10-310-154-702  
30 2513 42.0 1355 4 US-10-369-493-1388  
31 2513 42.0 1355 5 US-10-732-923-620  
32 2513 42.0 1355 5 US-10-732-923-22760  
33 2310 38.6 1035 4 US-10-369-493-12862  
34 2239.5 37.4 1190 4 US-10-332-447-4  
35 2239.5 37.4 1566 5 US-10-499-352A-523  
36 2231.5 37.3 1190 3 US-10-490-556-2  
37 2226.5 37.2 1190 4 US-09-964-295-2  
38 2226.5 37.2 1190 4 US-10-154-419-20  
39 2223 37.2 1251 3 US-09-964-295-4  
40 2223 37.2 1251 4 US-10-154-419-22  
41 2223 37.2 1251 4 US-10-295-027-1210  
42 2223 37.2 1251 4 US-10-188-832-70  
43 2223 37.2 1251 5 US-10-732-923-22729  
44 2223 37.2 1251 5 US-10-756-149-5289  
45 2221 37.1 1213 5 US-10-732-923-22589

ALIGNMENTS

RESULT 1

US-10-041-395-2  
; Sequence 2, Application US/10041395  
; Publication No. US20020119523A1  
; GENERAL INFORMATION:  
; APPLICANT: Curtiss, Rory A.J.  
; APPLICANT: Millennium Pharmaceuticals Inc.  
; TITLE OF INVENTION: 67073, A Human Phospholipid Transporter  
; TITLE OF INVENTION: Family Member and Uses Therefor  
; FILE REFERENCE: MPI2001-015P2R (M)  
; CURRENT APPLICATION NUMBER: US/10/041,395  
; CURRENT FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: 60/262,216  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/289,358  
; PRIOR FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-041-395-2

Query Match	99.5%	Score	5954	DB	4	Length	1176
Best Local Similarity	99.7%	Pred. No.	0				
Matches	1144	Conservative	2	Mismatches	2	Indels	0
Gaps	0						
Qy	1	MSRATSVGDQLEAPARTIYLNQPHLNKFRDNRISTAKYSVLTPLPRFLYEQIRRAANAFF	60				
Db	29	MSRATSVGDQLEAPARTIYLNQPHLNKFRDNRISTAKYSVLTPLPRFLYEQIRRAANAFF	88				
Qy	61	LFTALLOQIPDVSPGTGYTTLVPLIIITIAIGKEIVEDFRRHKADNANVKKTIIVLNG	120				
Db	89	LFTALLOQIPDVSPGTGYTTLVPLIIITIAIGKEIVEDFRRHKADNANVKKTIIVLNG	148				
Qy	121	MWHTIMKKEVAVGDIKVVNGQYLPADVLLSSSEPOAMCYVTANLDGETNLKIQGLS	180				
Db	149	MWHTIMKKEVAVGDIKVVNGQYLPADVLLSSSEPOAMCYVTANLDGETNLKIQGLS	208				
Qy	181	HTADMOTREVLMLKSGTIECBGNRHLVDFTGNLNDGKSLVALGPDQIILRGTLQRLNTQ	240				
Db	209	HTADMOTREVLMLKSGTIECBGNRHLVDFTGNLNDGKSLVALGPDQIILRGTLQRLNTQ	268				
Qy	241	WVFGIVVYTGHTDKLMQNSTKAPLKRNSVEKVTNVQILVLFGLLWVALVSSAGALYNNR	300				
Db	269	WVFGIVVYTGHTDKLMQNSTKAPLKRNSVEKVTNVQILVLFGLLWVALVSSAGALYNNR	328				
Qy	301	SHGKKNWYIKKQDTSNFGNLLTPIILYNNLIPISLLVTVLEVVKYTOALFINWDTDMY	360				

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OM protein - protein search, using sw model

Run on: March 29, 2006, 03:10:04 ; Search time 50 Seconds  
(without alignments)  
1898.234 Million cell updates/sec

Title: US-09-824-575A-2  
Perfect score: 5981  
Sequence: 1 MSRATSVGQLEAPRTIYL.....VSOEVRAYDTTKKSRKK 1148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues  
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/PCUS\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfilesi.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3191	53.4	615	2	US-09-949-016-9602
2	2223	37.2	1251	2	US-09-949-016-7784
3	1802	30.1	1177	2	US-09-795-927-2
4	1778	29.7	1426	2	US-09-710-092-14
5	1778	29.7	1426	2	US-10-231-354-14
6	1745.5	29.2	1270	2	US-09-710-092-10
7	1745.5	29.2	1270	2	US-10-231-354-10
8	1729	28.9	1395	2	US-09-949-016-7109
9	1393	23.3	822	2	US-09-248-796A-20787
10	1326.5	22.2	1056	2	US-09-710-092-6
11	1326.5	22.2	1056	2	US-10-231-354-6
12	1181.5	19.8	972	2	US-09-710-092-2
13	1181.5	19.8	972	2	US-10-231-354-2
14	1042	17.4	736	2	US-10-104-047-3774
15	947.5	15.8	818	2	US-09-248-796A-20792
16	869.5	14.5	324	2	US-09-248-796A-20753
17	852.5	14.3	578	2	US-09-710-092-16
18	852.5	14.3	578	2	US-10-231-354-16
19	820	13.7	422	2	US-09-710-092-12
20	820	13.7	422	2	US-10-231-354-12
21	814	13.6	622	2	US-09-270-767-44449
22	805.5	13.5	815	2	US-09-248-796A-20788
23	751.5	12.6	529	2	US-10-104-047-2137
24	637.5	10.7	570	2	US-09-248-796A-18607
25	539.5	9.0	451	2	US-09-248-796A-20754
26	534	8.9	374	2	US-09-795-927-4
27	503.5	8.4	255	2	US-09-270-767-33855

28	503.5	8.4	255	2	US-09-270-767-49072	Sequence 49072, A
29	425	7.1	225	2	US-09-248-796A-20752	Sequence 20752, A
30	422	7.1	331	2	US-09-248-796A-20795	Sequence 20795, A
31	408	6.8	1198	2	US-09-949-016-6109	Sequence 6109, Ap
32	406.5	6.8	185	2	US-09-248-796A-20789	Sequence 20789, A
33	401	6.7	208	2	US-09-710-092-8	Sequence 8, Appl1
34	401	6.7	208	2	US-10-231-354-8	Sequence 8, Appl1
35	391.5	6.5	1179	2	US-09-949-016-10545	Sequence 10545, A
36	390.5	6.5	239	2	US-09-270-767-59887	Sequence 59887, A
37	358.5	6.0	1225	2	US-09-949-016-9468	Sequence 9468, Ap
38	354	5.9	898	2	US-09-583-110-3327	Sequence 3327, Ap
39	354	5.9	916	2	US-09-107-433-2987	Sequence 2987, Ap
40	328	5.5	719	2	US-09-107-532A-5392	Sequence 5392, Ap
41	326	5.5	1141	2	US-09-949-016-9459	Sequence 9459, Ap
42	324	5.4	829	2	US-09-270-767-46176	Sequence 46176, A
43	305.5	5.1	690	2	US-09-949-016-8803	Sequence 8803, Ap
44	303	5.1	84	2	US-09-513-999C-6727	Sequence 6727, Ap
45	301.5	5.0	1031	2	US-09-949-016-7849	Sequence 7849, Ap

ALIGNMENTS

RESULT 1  
US-09-949-016-9602  
; Sequence 9602, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9602  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9602

Query Match	53.4%	Score 3191	DB 2	Length 615
Best Local Similarity	59.7%	Pred. No. 0		
Matches	613	Conservative	0	Mismatches 2
				Indels 0
				Gaps 0
Qy	534	KRMVIVRTSGRLRYCKGADNVIFRLSKDSKYMEETLCHLEFYFATEGRLTLCVAYAD	593	
Db	1	KRMVIVRTSGRLRYCKGADNVIFRLSKDSKYMEETLCHLEFYFATEGRLTLCVAYAD	60	
Qy	594	LSENEYEWLKVQEAETILKDRALRECEYIEIKNLLLGATAIEDRLQAGVPETIAT	653	
Db	61	LSENEYEWLKVQEAETILKDRALRECEYIEIKNLLLGATAIEDRLQAGVPETIAT	120	
Qy	654	LLKAKIKIWLTDGKQTAINIGYSCRLVSNMALLIKEDSLDAAITOHCTDLGNL	713	
Db	121	LLKAKIKIWLTDGKQTAINIGYSCRLVSNMALLIKEDSLDAAITOHCTDLGNL	180	
Qy	714	LGKENDVALLIDGHTLKVLSFEVRRSFLDLALSKAVICCRVSPLOKSEIVDVVKRVK	773	
Db	181	LGKENDVALLIDGHTLKVLSFEVRRSFLDLALSKAVICCRVSPLOKSEIVDVVKRVK	240	
Qy	774	AITLAIIGDANDVGMIOAHVGVGISGNEGQATNSDYAIAQPSYLEKLLVHGASYN	833	
Db	241	AITLAIIGDANDVGMIOAHVGVGISGNEGQATNSDYAIAQPSYLEKLLVHGASYN	300	
Qy	834	RVTKCILYCFYKNVLYIIELWFAFVNGFSGQILFERWCIGLYNVIPTALPPFTLGP	893	

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OM protein - protein search, using sw model  
Run on: March 29, 2006, 03:05:44 ; Search time 50 Seconds  
(without alignments)  
2209.137 Million cell updates/sec

Title: US-09-824-575A-2  
Perfect score: 5981  
Sequence: 1 MSRATSGDQLEAPARTIYL.....VSQEVIRAYDTTKKSRKK 1148

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4133	69.1	1149	T30869	probable adenosine
2	4107	68.7	1149	T18515	adenosinetriphosph
3	3793	63.4	729	T46328	probable adenosine
4	2640	44.1	1258	T40737	probable calcium-t
5	2513	42.0	1355	S51995	probable ATPase (H
6	2216.5	37.1	1123	C96622	probable ATPase F2
7	2090	34.9	1228	G96751	hypothetical prote
8	2085.5	34.9	1244	C96584	hypothetical prote
9	2032.5	34.0	1184	D86387	probable protein p
10	2032	34.0	1200	F96711	hypothetical prote
11	1991	33.3	1203	F86266	probable phospholi
12	1842	30.8	1571	S50669	hypothetical prote
13	1812.5	30.3	1402	S62557	probable calcium-t
14	1795	30.0	1612	S51243	probable ATPase (H
15	1701	28.4	1367	T38820	probable calcium-t
16	1582.5	26.5	1656	S54520	probable membrane
17	1574	26.3	1353	T26301	hypothetical prote
18	1524	25.5	632	T27057	hypothetical prote
19	1444	24.1	1553	S67483	adenosinetriphosph
20	1426.5	23.9	1454	C98175	protein T24H7.5a [
21	1424.5	23.8	1212	D88175	probable calcium-t
22	1229	20.5	1033	T39030	probable membrane
23	1194.5	20.0	1151	S48431	probable E1-E2 ATP
24	1192	19.9	1020	T42229	hypothetical prote
25	1167.5	19.5	1059	T21891	hypothetical prote
26	1146	19.2	221	T51867	hypothetical prote
27	1119	18.7	1864	T18485	hypothetical prote
28	985	16.5	626	D88601	protein Y49E10.11
29	938	15.7	1156	T14899	aminophospholipid

protein H06H21.10  
probable adenosine  
hypothetical prote  
cation-transportin  
Ca2+-transporting  
Ca2+-transporting  
calcium-transporti  
plasma membrane Ca  
Ca2+-transporting  
Ca2+-transporting  
cation-transportin  
cation-transportin  
Ca2+-transporting  
Ca2+-transporting  
Ca2+-transporting  
Ca2+-transporting

ALIGNMENTS

RESULT 1

T30869  
probable adenosinetriphosphatase (EC 3.6.1.3) - mouse  
N;Alternate names: chromaffin granule ATPase II; P-type ATPase  
C;Species: Mus musculus (house mouse)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30869  
R;Pradhan, D.; Blackman, C.F.; Williamson, P.; Schlegel, R.A.  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z20912  
A;Accession: T30869  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1149 <PRA>  
A;Cross-references: UNIPROT:P70704; UNIPARC:UPI000002773D; EMBL:U75321; NID:g1663647;  
C;Keywords: hydrolase

Query Match 69.1%; Score 4133; DB 2; Length 1149;  
Best Local Similarity 68.3%; Pred. No. 1.1e-280;  
Matches 781; Conservative 150; Mismatches 191; Indels 22; Gaps 4;

Qy	1	MSRATSGDQLEAPARTIYLNQPHANKFRDNRISTAKYSVLTPLPRELYEQIRRAANAF 60
Db	24	VSEKTSADQEE--VRTIFINQQLYFCNNHUSTAKYVITFPLRELYSQFRAANSFP 81
Qy	61	LFTALLQQIPDVSTGRYTYTLVPLIIILITAGIKVEIDFKRHKADNAVKNKKTIVLRNG 120
Db	82	LFTALLQQIPDVSTGRYTYTLVPLIIILITAGIKVEIDFKRHKADNAVKNKKTIVLRNG 141
Qy	121	MWHTIMKVEVAGDVKVNVNGQYLPADVLLSSSEPOAMCYVETANLDGETNLKIROGLS 180
Db	142	AWBIVHWEKVNVDGVIKGYIPADTVLLSSSEPOAMCYVETANLDGETNLKIROGLP 201
Qy	181	HTADMOTREVLMKLSGTIECEGNHLYDFTGNLNDGKSLVAGPQIILRGTLQRLNTQ 240
Db	202	ATSDIKDIDSLMRISGRICESEPNRHYDPVGNIRLDGHTGTPVUGAQIILRGTLQRLNTQ 261
Qy	241	WVGIVVYTGHTKLMONSTKAPLKRNVKVNQVLLVLFGLILLVMAVSSAGALYNNR 300
Db	262	WVGIVVYTGHTKLMONSTKAPLKRNVKVNQVLLVLFGLILLVMAVSSAGALYNNR 321
Qy	301	SHGKKNWYIKKMDTSDNFQVLLTPIILVNNLIPISLLVLEVVVKVTOALFINWDTMY 360
Db	322	RHSKDWYHLHYGGASNGFLNLTPIILVNNLIPISLLVLEVVVKVTOALFINWDTMY 381
Qy	361	YIGNDTPAMARTSNLNEELQVYLPQDKTGTLTCTNIMNFKKSIAGVYGHFPELAREP 420
Db	382	YEPTDTAAMARTSNLNEELQVYLPQDKTGTLTCTNIMNFKKSIAGVYGHFPELAREP 432
Qy	421	SSDDFCRMPPCSDCDPDPRLNIEDRHPTAPCQIEFLTLAVVCHTVVPEKGDNI 480
Db	433	QS90F-----GDEKTFNDPFLDLNQLNNHPTAPIICEFLTMVAVCHTAVPERGDKII 485